SEQUENCE LISTING

<110> GeneProt, Inc
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       Niknejad, Anne

<120> ENGINEERED HUMAN KUNITZ-TYPE PROTEASE INHIBITOR

<130> 5013-WO01

<150> US 60/358,683
<151> 2002-02-21

<160> 16

<170> PatentIn version 3.1

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Gly Asp Ile Gln Glu Pro Gly His Ala Glu Gly Ile Leu Gly Lys Pro
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Cys Pro Lys Ile Lys Val Glu Cys Glu Val Glu Glu Ile Asp Gln Cys
            35                  40                  45


Thr Lys Pro Arg Asp Cys Pro Glu Asn Met Lys Cys Cys Pro Phe Ser
        50                  55                  60


Cys Gly Lys Lys Cys Leu Asp Phe Arg Lys Asp Ile Cys Ser Met Pro
65                  70                  75                  80


Gln Glu Ala Gly Pro Cys Leu Ala Ser Ile Pro His Trp Trp Tyr Asn
                85                  90                  95


Lys Lys Thr Lys Ile Cys Ser Glu Phe Ile Tyr Gly Gly Cys Gln Gly
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Met Lys Cys Cys Pro Phe Ser Cys Gly Lys Lys Cys Leu Asp Phe Arg
            35                  40                  45


Lys Asp Ile Cys Ser Met Pro Gln Glu Ala Gly Pro Cys Leu Ala Ser
        50                  55                  60


Ile Pro His Trp Trp Tyr Asn Lys Lys Thr Lys Ile Cys Ser Glu Phe
65                  70                  75                  80


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   1               5                   10                  15
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               20                  25                  30
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gggaaagagg  ggagctattt  gaagtctctt  ggtaagagac  tcccttggtg  aatacaggca      2312

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tggacctaga  gctcatgaaa  tgaactaaga  aggagtagta  agcccaagga  agtctcccac      2432

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40                        45                50                  55
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Arg Lys
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gca gat ata tgc agt atg cca cag gag gct ggc ccc tgc ctg gcc tcc   6164
Asp Ile Cys Ser Met Pro Gln Glu Ala Gly Pro Cys Leu Ala Ser
    75              80                  85
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ata cca cac tgg tgg tac aat aaa aaa a act aag atc tgc tcc gaa ttc   6213
Ile Pro His Trp Trp Tyr Asn Lys Lys   Thr Lys Ile Cys Ser Glu Phe
    90              95                      100
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105             110             115                 120
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Ile Cys Leu Val Thr Cys Lys Lys Tyr His
            125             130
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ggctaagcta  gaataagtgc  aagtcccact  tgatcctctt  atgtagcttg  tttgggggca   9611

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catgtgggtg  ctgtgatcag  caggcccaga  taagctctga  ctgatagcca  gcatcaattt   9731

cagccatgca  aatgagatgc  ccaacccaat  agagccttca  gatggctgca  gccccagcag   9791

.acatctgact  gcaaccatgg  gaaagaccct  ataaaagaac  caccaagcag  attgcttccc   9851

agatggctga  cccacaatat  aaaatggttg  ctttaaagtg  ctaagttttc  agaaaattta   9911

ttcacagaat  aggtgatcaa  agatggaaac  gggctaggag  cagtggctca  cagctgtaat   9971

cccaggcact  ttgggagtcc  aaggcaggca  gataacttga  agtcagaagt  tcaagaccag  10031

cctggccaaa  acggcaaaac  cctgtctcta  ctaaaaatac  aaaaattagc  cagacatagt  10091

ggcgggcacc  tgtaatacca  cctactcggg  aggctggggc  aggagaatct  cttcagcccg  10151

ggaggcggag  gttgcagtga  gctgagattg  cgccactgca  ctccagagcg  agatttggtc  10211

tcaaaaaaaa  aaaagaaag   aaaaaaaga   tgaaaaggga  gtagaaggaa  ggatagggag  10271

agagaaagaa  gaaagagaca  cccataggac  tgggcaagat  aagaggatgc  caggcttgag  10331

aagggaacct  cacaacaggc  agcttgtcat  cacagcacac  caagacttgc  tatctcttgt  10391

caaataagtt  tgttgtttaa  tataacttgg  atcaaggggc  tctaaagagg  ctggaattca  10451

tttgctgttg  atgctgttgc  catctctgct  tccctctctt  tagaaagggc  tggtaaaact  10511

gattgtagaa  aactctaaag  gcactgcaaa  aaaaggttag  aattaataaa  caaatttatt  10571

aaagttacag  gatacaaaat  caacatacaa  aaatcaatag  caactttata  caccaagaac  10631

aatctcattt  ccatcagcgg  caacaacaac  aaaacactca  gtaattaact  caaccaaaga  10691

agtgaaaaac  ttatgcattg  acaattataa  aacatcgatg  aaggaaattt  aaaagacaca  10751
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aataaatgaa  aagacatcca  tgctcataga  ttagaagaat  caatgttgtc  aaaatgtcca  10811

cactacccaa  agcaatctac  agagcacatg  caatttctgc  caaaatgcca  atggcatttt  10871

ttacagaaac  ataaaaagca  atgctaaaat  tcatatggaa  ccacaaaaga  ccccaaattg  10931

ccaaaggaat  tttgaaaaag  aacagagctg  taagcaccac  atttcctgat  gtcaaattac  10991

attgcaaagc  tagagtaatc  aaaagagtgt  ggtactggca  taaaaacaga  aaagcagaca  11051

tacaggccaa  tggaacagaa  tagagaagcc  agaactaagc  ccacccattt  atggtcaatt  11111

gatctttgac  gagggtgtca  aaaacacaca  ataggcaaca  gaagatctct  ttaacaaatg  11171

gtgctgggaa  aactagatat  tcacatgcaa                                      11201
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<210>   4
<211>   30
<212>   PRT
<213>   Homo  Sapiens

<400>   4

Met Gly Leu Ser Gly Leu Leu Pro Ile Leu Val Pro Phe Ile Leu Leu
1               5                   10                  15


Gly Asp Ile Gln Glu Pro Gly His Ala Glu Gly Ile Leu Gly
            20                  25                  30


<210>   5
<211>   43
<212>   PRT
<213>   Homo  Sapiens

<400>   5

Pro Cys Pro Lys Ile Lys Val Glu Cys Glu Val Glu Glu Ile Asp Gln
1               5                   10                  15


Cys Thr Lys Pro Arg Asp Cys Pro Glu Asn Met Lys Cys Cys Pro Phe
            20                  25                  30


Ser Arg Gly Lys Lys Cys Leu Asp Phe Arg Lys
            35                  40


<210>   6
<211>   24
<212>   PRT
<213>   Homo  Sapiens

<400>   6

Asp Ile Cys Ser Met Pro Gln Glu Ala Gly Pro Cys Leu Ala Ser Ile
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1              5                10                15


Pro His Trp Trp Tyr Asn Lys Lys
                20


<210>  7
<211>  33
<212>  PRT
<213>  Homo Sapiens

<400>  7

Thr Lys Ile Cys Ser Glu Phe Ile Tyr Gly Gly Ser Gln Gly Asn Asn
1              5                10                15


Asn Asn Phe Gln Thr Glu Ala Ile Cys Leu Val Thr Cys Lys Lys Tyr
                20                  25                  30


His


<210>  8
<211>  1339
<212>  DNA
<213>  Homo Sapiens

<220>
<221>  misc_feature
<222>  (1)..(1339)
<223>  reconstructed cDNA from seqID 3


<220>
<221>  CDS
<222>  (1)..(294)
<223>


<220>
<221>  CDS
<222>  (296)..(394)
<223>


<220>
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<222>  (394)..(396)
<223>  potential stop codon


<220>
<221>  3'UTR
<222>  (397)..(1339)
<223>  partial
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<220>
<221>  polyA_signal
<222>  (1334)..(1339)
<223>

<400>   8
atg gga ctc tca gga ctt ctg cca atc ctg gta cca ttc atc ctt ttg          48
Met Gly Leu Ser Gly Leu Leu Pro Ile Leu Val Pro Phe Ile Leu Leu
1               5                   10                  15

ggg gac atc cag gaa cct ggg cac gct gaa ggc atc ctt ggc aag ccg          96
Gly Asp Ile Gln Glu Pro Gly His Ala Glu Gly Ile Leu Gly Lys Pro
                20                  25                  30

tgt ccc aaa atc aaa gtg gaa tgc gaa gtg gaa gaa ata gac cag tgt         144
Cys Pro Lys Ile Lys Val Glu Cys Glu Val Glu Glu Ile Asp Gln Cys
            35                  40                  45

acc aaa ccc aga gat tgc cca gaa aac atg aag tgt tgc ccg ttc agc         192
Thr Lys Pro Arg Asp Cys Pro Glu Asn Met Lys Cys Cys Pro Phe Ser
        50                  55                  60

cgt gga aag aaa tgt tta gac ttc aga aag gat ata tgc agt atg cca         240
Arg Gly Lys Lys Cys Leu Asp Phe Arg Lys Asp Ile Cys Ser Met Pro
65                  70                  75                  80

cag gag gct ggc ccc tgc ctg gcc tcc ata cca cac tgg tgg tac aat         288
Gln Glu Ala Gly Pro Cys Leu Ala Ser Ile Pro His Trp Trp Tyr Asn
                85                  90                  95

aaa aaa a act aag atc tgc tcc gaa ttc atc tat ggc ggt agc cag ggg       337
Lys Lys    Thr Lys Ile Cys Ser Glu Phe Ile Tyr Gly Gly Ser Gln Gly
                100                 105                 110

aac aat aac aac ttc caa act gaa gct atc tgt ctg gtc acc tgc aaa         385
Asn Asn Asn Asn Phe Gln Thr Glu Ala Ile Cys Leu Val Thr Cys Lys
        115                 120                 125

aaa tac cat aagtcccaga ggtcccggtc tcctgtgctc accaaggcca               434
Lys Tyr His
    130

cactgggagg tctgggtgtt ggctggtcta ttccaagacc tgggtggcgc tggggatgac      494

aaaaccagct ccaatgcaga agtataagta gaaggatatt ttgggaaaga gggtgggaag      554

ggagggatta gtcaaaggga tattggcaag tatgaggtga gtagtgggtg tagagagaaa      614

acagaagtgg tggagtatcc cagaccaggt cagacggaag cccggtaaac ccagcccagc      674

cctgggcacc attcatcagc caatcattat agtcctttac ttctcactaa accttgttgc      734

tacttctctt cctttgaaag gttatttcta accagggcaa ccacatactt tattggccaa      794

accaaatcac ttttgaaagt gtctcaaggt gaggtgccat taattattac actgagacaa      854

caggcataaa ctgggactct actggacaag tcagaactca tgatcattct aggagccccc      914

aaactcacct tcattccatt cctgcccaaa gatgtaaaaa tgatcccacc tccttttttcc     974
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cattaggtgc aagatttggt tcctaatgtg gtcagggtcc aagcatctca cccttattc    1034

ttctgcttca caggtcagcc ttactttata ccataaggag gagcttgaat aacctccagg    1094

atttggctca taatccaggc ctctctccac gtgtgcctga ttgatgctcc aaattggctt    1154

ccacgggcca aaccttggct gttccagaaa ctgaacccca ggaattgctt acacactttc    1214

ttccagcgta gcatctcttc aaacacaatg ctcttcccct tgaccacttc tcagtatgaa    1274

actctatgtc ttcaactttc agacccccca tttatttgta tgaaggcttc agttgcctta    1334

ataaa                                                                1339
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<210> 9
<211> 98
<212> PRT
<213> Homo Sapiens

<400> 9

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Met Gly Leu Ser Gly Leu Leu Pro Ile Leu Val Pro Phe Ile Leu Leu
1               5                   10                  15


Gly Asp Ile Gln Glu Pro Gly His Ala Glu Gly Ile Leu Gly Lys Pro
            20                  25                  30


Cys Pro Lys Ile Lys Val Glu Cys Glu Val Glu Glu Ile Asp Gln Cys
        35                  40                  45


Thr Lys Pro Arg Asp Cys Pro Glu Asn Met Lys Cys Cys Pro Phe Ser
    50                  55                  60


Arg Gly Lys Lys Cys Leu Asp Phe Arg Lys Asp Ile Cys Ser Met Pro
65                  70                  75                  80


Gln Glu Ala Gly Pro Cys Leu Ala Ser Ile Pro His Trp Trp Tyr Asn
                85                  90                  95


Lys Lys
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<210> 10
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 10

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Thr Lys Ile Cys Ser Glu Phe Ile Tyr Gly Gly Ser Gln Gly Asn Asn
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1                 5                    10                      15


Asn Asn Phe Gln Thr Glu Ala Ile Cys Leu Val Thr Cys Lys Lys Tyr
            20                  25                  30


His
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<210>  11
<211>  396
<212>  DNA
<213>  Homo Sapiens

<220>
<221>  misc_feature
<222>  (1)..(396)
<223>  reconstructed cDNA for seqID 1


<220>
<221>  CDS
<222>  (1)..(396)
<223>


<400>  11
atg gga ctc tca gga ctt ctg cca atc ctg gta cca ttc atc ctt ttg      48
Met Gly Leu Ser Gly Leu Leu Pro Ile Leu Val Pro Phe Ile Leu Leu
1               5                   10                  15

ggg gac atc cag gaa cct ggg cac gct gaa ggc atc ctt ggc aag ccg      96
Gly Asp Ile Gln Glu Pro Gly His Ala Glu Gly Ile Leu Gly Lys Pro
                20                  25                  30

tgt ccc aaa atc aaa gtg gaa tgc gaa gtg gaa gaa ata gac cag tgt     144
Cys Pro Lys Ile Lys Val Glu Cys Glu Val Glu Glu Ile Asp Gln Cys
                35                  40                  45

acc aaa ccc aga gat tgc cca gaa aac atg aag tgt tgc ccg ttc agc     192
Thr Lys Pro Arg Asp Cys Pro Glu Asn Met Lys Cys Cys Pro Phe Ser
      50                  55                  60

tgt gga aag aaa tgt tta gac ttc aga aag gat ata tgc agt atg cca     240
Cys Gly Lys Lys Cys Leu Asp Phe Arg Lys Asp Ile Cys Ser Met Pro
65                  70                  75                  80

cag gag gct ggc ccc tgc ctg gcc tcc ata cca cac tgg tgg tac aat     288
Gln Glu Ala Gly Pro Cys Leu Ala Ser Ile Pro His Trp Trp Tyr Asn
                85                  90                  95

aaa aaa act aag atc tgc tcc gaa ttc atc tat ggc ggt tgc cag ggg     336
Lys Lys Thr Lys Ile Cys Ser Glu Phe Ile Tyr Gly Gly Cys Gln Gly
                100                 105                 110

aac aat aac aac ttc caa act gaa gct atc tgt ctg gtc acc tgc aaa     384
Asn Asn Asn Asn Phe Gln Thr Glu Ala Ile Cys Leu Val Thr Cys Lys
            115                 120                 125
```

```
aaa tac cat taa                                          396
Lys Tyr His
    130
```

```
<210>   12
<211>   131
<212>   PRT
<213>   Homo Sapiens

<400>   12
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```
Met Gly Leu Ser Gly Leu Leu Pro Ile Leu Val Pro Phe Ile Leu Leu
1               5               10              15
```

```
Gly Asp Ile Gln Glu Pro Gly His Ala Glu Gly Ile Leu Gly Lys Pro
            20              25              30
```

```
Cys Pro Lys Ile Lys Val Glu Cys Glu Val Glu Glu Ile Asp Gln Cys
        35              40              45
```

```
Thr Lys Pro Arg Asp Cys Pro Glu Asn Met Lys Cys Cys Pro Phe Ser
    50              55              60
```

```
Cys Gly Lys Lys Cys Leu Asp Phe Arg Lys Asp Ile Cys Ser Met Pro
65              70              75              80
```

```
Gln Glu Ala Gly Pro Cys Leu Ala Ser Ile Pro His Trp Trp Tyr Asn
            85              90              95
```

```
Lys Lys Thr Lys Ile Cys Ser Glu Phe Ile Tyr Gly Gly Cys Gln Gly
            100             105             110
```

```
Asn Asn Asn Asn Phe Gln Thr Glu Ala Ile Cys Leu Val Thr Cys Lys
        115             120             125
```

```
Lys Tyr His
    130
```

```
<210>   13
<211>   133
<212>   PRT
<213>   Homo sapiens

<400>   13
```

```
Met Gly Ser Ser Gly Leu Leu Ser Leu Leu Val Leu Phe Val Leu Leu
1               5               10              15
```

```
Ala Asn Val Gln Gly Pro Gly Leu Thr Asp Trp Leu Phe Pro Arg Arg
             20              25              30

Cys Pro Lys Ile Arg Glu Glu Cys Glu Phe Gln Glu Arg Asp Val Cys
         35              40              45

Thr Lys Asp Arg Gln Cys Gln Asp Asn Lys Lys Cys Cys Val Phe Ser
     50              55              60

Cys Gly Lys Lys Cys Leu Asp Leu Lys Gln Asp Val Cys Glu Met Pro
65              70              75              80

Lys Glu Thr Gly Pro Cys Leu Ala Tyr Phe Leu His Trp Trp Tyr Asp
             85              90              95

Lys Lys Asp Asn Thr Cys Ser Met Phe Val Tyr Gly Gly Cys Gln Gly
             100             105             110

Asn Asn Asn Asn Phe Gln Ser Lys Ala Asn Cys Leu Asn Thr Cys Lys
         115             120             125

Asn Lys Arg Phe Pro
     130
```

```
<210>   14
<211>   134
<212>   PRT
<213>   Mus musculus

<400>   14
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```
Met Lys Leu Ser Gly Phe Val Ser Ile Leu Val Leu Phe Gly Leu Leu
1               5               10              15

Ala Arg Val Gln Gly Pro Ser Leu Ala Asp Leu Leu Phe Pro Arg Arg
             20              25              30

Cys Pro Arg Phe Arg Glu Glu Cys Glu His Gln Glu Arg Asp Leu Cys
         35              40              45

Thr Arg Asp Arg Asp Cys Pro Lys Lys Glu Lys Cys Cys Val Phe Asn
     50              55              60

Cys Gly Lys Lys Cys Leu Asn Pro Gln Gln Asp Ile Cys Ser Leu Pro
65              70              75              80
```

```
Lys Asp Ser Gly Tyr Cys Met Ala Tyr Phe Arg Arg Trp Trp Phe Asn
              85                  90                  95

Lys Glu Asn Ser Thr Cys Gln Val Phe Ile Tyr Gly Gly Cys Gln Gly
              100                 105                 110

Asn Asn Asn Asn Phe Gln Ser Gln Ser Ile Cys Gln Asn Ala Cys Glu
          115                 120                 125

Lys Lys Ser Ser Leu Thr
      130


<210>   15
<211>   131
<212>   PRT
<213>   Homo sapiens

<400>   15

Met Gly Leu Ser Gly Leu Leu Pro Ile Leu Val Pro Phe Ile Leu Leu
1               5               10                  15

Gly Asp Ile Gln Glu Pro Gly His Ala Glu Gly Ile Leu Gly Lys Pro
              20                  25                  30

Cys Pro Lys Ile Lys Val Glu Cys Glu Val Glu Glu Ile Asp Gln Cys
          35              40                  45

Thr Lys Pro Arg Asp Cys Pro Glu Asn Met Lys Cys Cys Pro Phe Ser
      50              55                  60

Arg Gly Lys Lys Cys Leu Asp Phe Arg Lys Asp Ile Cys Ser Met Pro
65                  70                  75                  80

Gln Glu Ala Gly Pro Cys Leu Ala Ser Ile Pro His Trp Trp Tyr Asn
              85                  90                  95

Lys Lys Thr Lys Ile Cys Ser Glu Phe Ile Tyr Gly Gly Ser Gln Gly
              100                 105                 110

Asn Asn Asn Asn Phe Gln Thr Glu Ala Ile Cys Leu Val Thr Cys Lys
          115                 120                 125

Lys Tyr His
      130
```

<210> 16
<211> 136
<212> PRT
<213> Mus musculus

<400> 16

Met Arg Leu Trp Gly Leu Leu Pro Phe Leu Val Pro Phe Ile Leu Leu
1   5   10   15

Trp Ser Ile Gln Glu Pro Glu Leu Ala Glu Gly Phe Phe Ile Arg Thr
            20   25   30

Cys Pro Arg Val Arg Val Lys Cys Glu Val Glu Glu Arg Asn Glu Cys
        35   40   45

Thr Arg His Arg Gln Cys Pro Asn Lys Lys Arg Cys Cys Leu Phe Ser
    50   55   60

Cys Gly Lys Lys Cys Met Asp Leu Arg Gln Asp Val Cys Ser Leu Pro
65   70   75   80

Gln Asp Pro Gly Pro Cys Leu Ala Tyr Leu Pro Arg Trp Trp Tyr Asn
                85   90   95

Gln Glu Thr Asp Leu Cys Thr Glu Phe Ile Tyr Gly Gly Cys Gln Gly
                100   105   110

Asn Pro Asn Asn Phe Pro Ser Glu Gly Ile Cys Thr Val Val Cys Lys
        115   120   125

Lys Lys Gln Met Ser Ser Trp Ile
    130   135